Molecular Biology

AN EXPRESSED SEQUENCE FROM SEA URCHIN COLEOMOCYTES RESEMBLES THE TIE-1 AND TIE-2 GENES OF VERTEBRATES. <u>Jatinder K. Dhillon</u>, and Margaret E. Stevens*, Ripon College, Department of Biology, Ripon, WI 54971, <u>DhillonJ@ripon.edu</u>

Receptor tyrosine kinases (RTKs) are signaling molecules that often are involved in control of cell growth and proliferation. This study investigates a presumed RTK (EST059) expressed in the coelomocytes of the sea urchin Strongylocentrotus purpuratus. The library from which the gene was obtained used a pSPORT vector and some clones were subcloned in a Bluescript vector. Inserts were sequenced using primers from the cloning vectors and internal primers. The 4.7-kb sequence was analyzed using online databases and BLASTX, CLUSTAL, and SMART. An open reading frame of 4200 bp, with a signaling sequence at the 5' end and a second transmembrane region suggests that the protein product is a membrane-bound protein. The amino acid sequence shows significant homology to vertebrate tie-1 and tie-2 proteins, including a highly conserved cytoplasmic RTK domain and a complex extracellular domain containing an immunoglobulin-like (Ig) motif, three epidermal growth factor (EGF) motifs, a second Ig motif, and four fibronectin III motifs. The *tie* proteins of vertebrates are part of cell signaling pathways important in the formation of blood vessels, which are lacking in sea urchins. They also play a role in hematopoiesis, and sea urchin coelomocytes perform many of the functions of vertebrate white blood cells. In conclusion, the EST059 sequence was characterized and compared to the vertebrate *tie* proteins.